

Rec'd PCT/PTO 19 SEP 2005

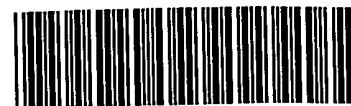
10/521916

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/521, 916
Source: PCT
Date Processed by STIC: 09/19/2005

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/521,916

DATE: 09/19/2005

TIME: 14:12:07

Input Set : A:\Sequence listing-US format.txt

Output Set: N:\CRF4\09192005\J521916.raw

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3 <110> APPLICANT: Matuschek, Markus
4   Hauer, Bernhard
5   Schmid, Rolf
6   Kauffmann, Isabelle
7   Blasco, Francesca
8   Schmidt-Dannert, Claudia
10 <120> TITLE OF INVENTION: Process for the biotransformation of carotenoids
12 <130> FILE REFERENCE: 13111-00001-US
14 <140> CURRENT APPLICATION NUMBER: 10/521,916
15 <141> CURRENT FILING DATE: 2005-01-20
17 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/008199
18 <151> PRIOR FILING DATE: 2003-07-25
20 <150> PRIOR APPLICATION NUMBER: DE 102 34 126.5
21 <151> PRIOR FILING DATE: 2002-07-26
23 <160> NUMBER OF SEQ ID NOS: 12
25 <170> SOFTWARE: PatentIn Ver. 3.3
27 <210> SEQ ID NO: 1
29 <211> LENGTH: 1170
31 <212> TYPE: DNA
33 <213> ORGANISM: Thermus thermophilus
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37 <221> NAME/KEY: CDS
39 <222> LOCATION: (1)..(1170)
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44   1           5           10           15
46 cag caa gat ccc ctc gcc gtc ctg ctg gcg tgg ggc cgg gcc cac ccc   96
47 Gln Gln Asp Pro Leu Ala Val Leu Leu Ala Trp Gly Arg Ala His Pro
48   20           25           30
50 cgg ctc ttc ctt ccc ctg ccc cgc ttc ccc ctg gcc ctg atc ttt gac   144
51 Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro Leu Ala Leu Ile Phe Asp
52   35           40           45
54 ccc gag ggg gtg gag ggg gcg ctc ctc gcc gag ggg acc acc aag gcc   192
55 Pro Glu Gly Val Glu Gly Ala Leu Leu Ala Glu Gly Thr Thr Lys Ala
56   50           55           60
58 acc ttc cag tac cgg gcc ctc tcc cgc ctc acg ggg agg ggc ctc ctc   240
59 Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu Thr Gly Arg Gly Leu Leu
60   65           70           75           80
62 acc gac tgg ggg gaa agc tgg aag gag gcg cgc aag gcc ctc aaa gac   288
63 Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala Arg Lys Ala Leu Lys Asp
64   85           90           95
66 ccc ttc ctg ccg aag aac gtc cgc ggc tac cgg gag gcc atg gag gag   336

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67 Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr Arg Glu Ala Met Glu Glu
68          100          105          110
70 gag gcc cgg gcc ttc ttc ggg gag tgg cgg ggg gag gag cgg gac ctg 384
71 Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg Gly Glu Glu Arg Asp Leu
72          115          120          125
74 gac cac gag atg ctc gcc ctc tcc ctg cgc ctc ctc ggg cgg gcc ctc 432
75 Asp His Glu Met Leu Ala Leu Ser Leu Arg Leu Leu Gly Arg Ala Leu
76          130          135          140
78 ttc ggg aag ccc ctc tcc cca agc ctc gcg gag cac gcc ctt aag gcc 480
79 Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala Glu His Ala Leu Lys Ala
80 145          150          155          160
82 ctg gac cgg atc atg gcc cag acc agg agc ccc ctg gcc ctc ctg gac 528
83 Leu Asp Arg Ile Met Ala Gln Thr Arg Ser Pro Leu Ala Leu Leu Asp
84          165          170          175
86 ctg gcc gcc gaa gcc cgc ttc cgg aag gac cgg ggg gcc ctc tac cgc 576
87 Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp Arg Gly Ala Leu Tyr Arg
88          180          185          190
90 gag gcg gaa gcc ctc atc gtc cac ccg ccc ctc tcc cac ctt ccc cga 624
91 Glu Ala Glu Ala Leu Ile Val His Pro Pro Leu Ser His Leu Pro Arg
92          195          200          205
94 gag cgc gcc ctg agc gag gcc gtg acc ctc ctg gtg gcg ggc cac gag 672
95 Glu Arg Ala Leu Ser Glu Ala Val Thr Leu Leu Val Ala Gly His Glu
96          210          215          220
98 acg gtg gcg agc gcc ctc acc tgg tcc ttt ctc ctc ctc tcc cac cgc 720
99 Thr Val Ala Ser Ala Leu Thr Trp Ser Phe Leu Leu Leu Ser His Arg
100 225          230          235          240
102 ccg gac tgg cag aag cgg gtg gcc gag agc gag gag gcg gcc ctc gcc 768
103 Pro Asp Trp Gln Lys Arg Val Ala Glu Ser Glu Glu Ala Ala Leu Ala
104          245          250          255
106 gcc ttc cag gag gcc ctg agg ctc tac ccc ccc gcc tgg atc ctc acc 816
107 Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro Pro Ala Trp Ile Leu Thr
108          260          265          270
110 cgg agg ctg gaa agg ccc ctc ctc ctg gga gag gac cgg ctc ccc ccg 864
111 Arg Arg Leu Glu Arg Pro Leu Leu Gly Glu Asp Arg Leu Pro Pro
112          275          280          285
114 ggc acc acc ctg gtc ctc tcc ccc tac gtg acc cag agg ctc cac ttc 912
115 Gly Thr Thr Leu Val Leu Ser Pro Tyr Val Thr Gln Arg Leu His Phe
116          290          295          300
118 ccc gat ggg gag gcc ttc cgg ccc gag cgc ttc ctg gag gaa agg ggg 960
119 Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg Phe Leu Glu Glu Arg Gly
120 305          310          315          320
122 acc cct tcg ggg cgc tac ttc ccc ttt ggc ctg ggg cag agg ctc tgc 1008
123 Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly Leu Gly Gln Arg Leu Cys
124          325          330          335
126 ctg ggg cgg gac ttc gcc ctc ctc gag ggc ccc atc gtc ctc agg gcc 1056
127 Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly Pro Ile Val Leu Arg Ala
128          340          345          350
130 ttc ttc cgc cgc ttc cgc cta gac ccc ctc ccc ttc ccc cgg gtc ctc 1104
131 Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu Pro Phe Pro Arg Val Leu

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132          355          360          365
134 gcc cag gtc acc ctg agg ccc gaa ggc ggg ctt ccc gcg cgg cct agg 1152
135 Ala Gln Val Thr Leu Arg Pro Glu Gly Gly Leu Pro Ala Arg Pro Arg
136          370          375          380          1170
138 gag gag gtg cgg gcg tga
139 Glu Glu Val Arg Ala
140 385
143 <210> SEQ ID NO: 2
145 <211> LENGTH: 389
147 <212> TYPE: PRT
149 <213> ORGANISM: Thermus thermophilus
151 <400> SEQUENCE: 2
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153 1 5 10 15
155 Gln Gln Asp Pro Leu Ala Val Leu Leu Ala Trp Gly Arg Ala His Pro
156 20 25 30
158 Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro Leu Ala Leu Ile Phe Asp
159 35 40 45
161 Pro Glu Gly Val Glu Gly Ala Leu Leu Ala Glu Gly Thr Thr Lys Ala
162 50 55 60
164 Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu Thr Gly Arg Gly Leu Leu
165 65 70 75 80
167 Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala Arg Lys Ala Leu Lys Asp
168 85 90 95
170 Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr Arg Glu Ala Met Glu Glu
171 100 105 110
173 Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg Gly Glu Glu Arg Asp Leu
174 115 120 125
176 Asp His Glu Met Leu Ala Leu Ser Leu Arg Leu Leu Gly Arg Ala Leu
177 130 135 140
179 Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala Glu His Ala Leu Lys Ala
180 145 150 155 160
182 Leu Asp Arg Ile Met Ala Gln Thr Arg Ser Pro Leu Ala Leu Leu Asp
183 165 170 175
185 Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp Arg Gly Ala Leu Tyr Arg
186 180 185 190
188 Glu Ala Glu Ala Leu Ile Val His Pro Pro Leu Ser His Leu Pro Arg
189 195 200 205
191 Glu Arg Ala Leu Ser Glu Ala Val Thr Leu Leu Val Ala Gly His Glu
192 210 215 220
194 Thr Val Ala Ser Ala Leu Thr Trp Ser Phe Leu Leu Leu Ser His Arg
195 225 230 235 240
197 Pro Asp Trp Gln Lys Arg Val Ala Glu Ser Glu Glu Ala Ala Leu Ala
198 245 250 255
200 Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro Pro Ala Trp Ile Leu Thr
201 260 265 270
203 Arg Arg Leu Glu Arg Pro Leu Leu Gly Glu Asp Arg Leu Pro Pro
204 275 280 285
206 Gly Thr Thr Leu Val Leu Ser Pro Tyr Val Thr Gln Arg Leu His Phe

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207      290      295      300
209 Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg Phe Leu Glu Glu Arg Gly
210 305      310      315      320
212 Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly Leu Gly Gln Arg Leu Cys
213      325      330      335
215 Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly Pro Ile Val Leu Arg Ala
216      340      345      350
218 Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu Pro Phe Pro Arg Val Leu
219      355      360      365
221 Ala Gln Val Thr Leu Arg Pro Glu Gly Gly Leu Pro Ala Arg Pro Arg
222      370      375      380
224 Glu Glu Val Arg Ala
225 385
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230 <211> LENGTH: 1188
232 <212> TYPE: DNA
234 <213> ORGANISM: Artificial sequence
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238 <221> NAME/KEY: misc_feature
240 <222> LOCATION: (4)..(21)
242 <223> OTHER INFORMATION: His tag
244 <220> FEATURE:
246 <223> OTHER INFORMATION: Description of the artificial sequence: N-terminal
247 his tagged
249 <220> FEATURE:
251 <221> NAME/KEY: CDS
253 <222> LOCATION: (1)..(1188)
255 <400> SEQUENCE: 3
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258 1 5 10 15
260 ccc tac ctg aaa gac ctc cag caa gat ccc ctc gcc gtc ctg ctg gcg 96
261 Pro Tyr Leu Lys Asp Leu Gln Gln Asp Pro Leu Ala Val Leu Leu Ala
262 20 25 30
264 tgg ggc cgg gcc cac ccc cgg ctc ttc ctt ccc ctg ccc cgc ttc ccc 144
265 Trp Gly Arg Ala His Pro Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro
266 35 40 45
268 ctg gcc ctg atc ttt gac ccc gag ggg gtg gag ggg gcg ctc ctc gcc 192
269 Leu Ala Leu Ile Phe Asp Pro Glu Gly Val Glu Gly Ala Leu Leu Ala
270 50 55 60
272 gag ggg acc acc aag gcc acc ttc cag tac cgg gcc ctc tcc cgc ctc 240
273 Glu Gly Thr Thr Lys Ala Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu
274 65 70 75 80
276 acg ggg agg ggc ctc ctc acc gac tgg ggg gaa agc tgg aag gag gcg 288
277 Thr Gly Arg Gly Leu Leu Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala
278 85 90 95
280 cgc aag gcc ctc aaa gac ccc ttc ctg ccg aag aac gtc cgc ggc tac 336
281 Arg Lys Ala Leu Lys Asp Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr
282 100 105 110

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284	cgg	gag	gcc	atg	gag	gag	gag	gcc	cgg	gcc	ttc	ttc	ggg	gag	tgg	cgg	384
285	Arg	Glu	Ala	Met	Glu	Glu	Glu	Ala	Arg	Ala	Phe	Phe	Gly	Glu	Trp	Arg	
286			115					120					125				
288	ggg	gag	gag	cgg	gac	ctg	gac	cac	gag	atg	ctc	gcc	ctc	tcc	ctg	cgc	432
289	Gly	Glu	Glu	Arg	Asp	Leu	Asp	His	Glu	Met	Leu	Ala	Leu	Ser	Leu	Arg	
290		130					135					140					
292	ctc	ctc	ggg	cgg	gcc	ctc	ttc	ggg	aag	ccc	ctc	tcc	cca	agc	ctc	gcg	480
293	Leu	Leu	Gly	Arg	Ala	Leu	Phe	Gly	Lys	Pro	Leu	Ser	Pro	Ser	Leu	Ala	
294	145					150					155					160	
296	gag	cac	gcc	ctt	aag	gcc	ctg	gac	cgg	atc	atg	gcc	cag	acc	agg	agc	528
297	Glu	His	Ala	Leu	Lys	Ala	Leu	Asp	Arg	Ile	Met	Ala	Gln	Thr	Arg	Ser	
298					165				170						175		
300	ccc	ctg	gcc	ctc	ctg	gac	ctg	gcc	gcc	gaa	gcc	cgc	ttc	cgg	aag	gac	576
301	Pro	Leu	Ala	Leu	Leu	Asp	Leu	Ala	Ala	Glu	Ala	Arg	Phe	Arg	Lys	Asp	
302					180				185				190				
304	cgg	ggg	gcc	ctc	tac	cgc	gag	gag	gaa	gcc	ctc	atc	gtc	cac	ccg	ccc	624
305	Arg	Gly	Ala	Leu	Tyr	Arg	Glu	Ala	Glu	Ala	Leu	Ile	Val	His	Pro	Pro	
306			195				200					205					
308	ctc	tcc	cac	ctt	ccc	cga	gag	cgc	gcc	ctg	agc	gag	gcc	gtg	acc	ctc	672
309	Leu	Ser	His	Leu	Pro	Arg	Glu	Arg	Ala	Leu	Ser	Glu	Ala	Val	Thr	Leu	
310		210				215					220						
312	ctg	gtg	gag	ggc	cac	gag	acg	gtg	gag	agc	gcc	ctc	acc	tgg	tcc	ttt	720
313	Leu	Val	Ala	Gly	His	Glu	Thr	Val	Ala	Ser	Ala	Leu	Thr	Trp	Ser	Phe	
314	225				230				235							240	
316	ctc	ctc	ctc	tcc	cac	cgc	ccg	gac	tgg	cag	aag	cgg	gtg	gcc	gag	agc	768
317	Leu	Leu	Leu	Ser	His	Arg	Pro	Asp	Trp	Gln	Lys	Arg	Val	Ala	Glu	Ser	
318					245				250						255		
320	gag	gag	gag	gcc	ctc	gcc	gcc	ttc	cag	gag	gcc	ctg	agg	ctc	tac	ccc	816
321	Glu	Glu	Ala	Ala	Leu	Ala	Ala	Phe	Gln	Glu	Ala	Leu	Arg	Leu	Tyr	Pro	
322			260					265					270				
324	ccc	gcc	tgg	atc	ctc	acc	cgg	agg	ctg	gaa	agg	ccc	ctc	ctc	ctg	gga	864
325	Pro	Ala	Trp	Ile	Leu	Thr	Arg	Arg	Leu	Glu	Arg	Pro	Leu	Leu	Leu	Gly	
326			275				280						285				
328	gag	gac	cgg	ctc	ccc	ccg	ggc	acc	ctg	gtc	ctc	tcc	ccc	tac	gtg		912
329	Glu	Asp	Arg	Leu	Pro	Pro	Gly	Thr	Thr	Leu	Val	Leu	Ser	Pro	Tyr	Val	
330		290				295					300						
332	acc	cag	agg	ctc	cac	ttc	ccc	gat	ggg	gag	gcc	ttc	cgg	ccc	gag	cgc	960
333	Thr	Gln	Arg	Leu	His	Phe	Pro	Asp	Gly	Glu	Ala	Phe	Arg	Pro	Glu	Arg	
334	305				310						315					320	
336	ttc	ctg	gag	gaa	agg	ggg	acc	cct	tcg	ggg	cgc	tac	ttc	ccc	ttt	ggc	1008
337	Phe	Leu	Glu	Glu	Arg	Gly	Thr	Pro	Ser	Gly	Arg	Tyr	Phe	Pro	Phe	Gly	
338					325				330						335		
340	ctg	ggg	cag	agg	ctc	tgc	ctg	ggg	cgg	gac	ttc	gcc	ctc	ctc	gag	ggc	1056
341	Leu	Gly	Gln	Arg	Leu	Cys	Leu	Gly	Arg	Asp	Phe	Ala	Leu	Leu	Glu	Gly	
342			340					345					350				
344	ccc	atc	gtc	ctc	agg	gcc	ttc	ttc	cgc	cgc	ttc	cgc	cta	gac	ccc	ctc	1104
345	Pro	Ile	Val	Leu	Arg	Ala	Phe	Phe	Arg	Arg	Phe	Arg	Leu	Asp	Pro	Leu	
346			355				360						365				
348	ccc	ttc	ccc	cgg	gtc	ctc	gcc	cag	gtc	acc	ctg	agg	ccc	gaa	ggc	ggg	1152

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/521,916

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